

REMARKS

STATUS OF CLAIMS

Claims 2-9 are pending.

The Abstracted is objected to for informalities as indicated by the Examiner.

Claims 2-7 are rejected under 35 USC 112, second paragraph, for indefiniteness.

Claims 8-9 are rejected under 35 USC 103(a) as being unpatentable over Kawanishi (US Patent No. 5,598,350), Attwood (J. Chem. Inf. Comput. Sci. 1997, vol. 3, pp. 417-424), and in view of Marr (US Patent No. 5,701,256). Marr is newly cited, and thus, newly relied upon.

Claim 2 is amended.

Thus, claims 2-9 remain pending for reconsideration, which is respectfully requested.

No new matter has been asserted in this Amendment. The foregoing rejections are hereby traversed.

IN THE ABSTRACT

The Abstract is replaced with a new Abstract (attached hereto as a separate sheet) taking into consideration the Examiner's comments. Withdrawal of the objection to the Abstract is respectfully requested.

35 USC 112, SECOND PARAGRAPH, REJECTIONS

Claims 2-7 are rejected under 35 USC 112, second paragraph, for indefiniteness. Claim 2 is amended to improve form. Support for the claim amendments can be found, for example, in page 8, last paragraph, through page 9, 2nd to last paragraph. Withdrawal of the rejections of claims 2-7 and allowance of claims 2-7 is respectfully requested.

35 USC 103 REJECTIONS

Claims 8-9 are rejected under 35 USC 103(a) as being unpatentable over Kawanishi (US Patent No. 5,598,350), Attwood (J. Chem. Inf. Comput. Sci. 1997, vol. 3, pp. 417-424), and in view of Marr (US Patent No. 5,701,256). Marr is newly cited, and thus, newly relied upon.

The Examiner relies on Marr for the recited feature, "designating interactively ... a motif extraction range." See, page 4, last paragraph, of the Office Action. The Examiner appears to assert that an interactive input parameter is obvious.

However, the patentably distinguishing features of the claimed invention are (1) to interactively designate the motif extraction range based on gene arrangement information input as an object to be clarified, (2) to retrieve from a database the gene arrangement information including the motif as a part thereof, and (3) to add the retrieved gene arrangement information to the input gene arrangement information. In particular, the patentably distinguishing features of the invention are the recitations,

... means for an operator interactively designating ... a motif extraction range in the input gene arrangement information;

...

... means for retrieving, based on the motif extracted from the input gene arrangement information, gene arrangement information including the extracted motif ... ; and

... means for adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information.

Therefore, the claimed combination of interactively designating a motif extraction and adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information, is patentably distinguishing over the combination of Kwanishi, Attwood, and Marr.

First, regarding the recitation, "an operator interactively designating ... a motif extraction range in the input gene arrangement information," the Examiner relies on Kawashini and Marr, and the Examiner admits that Attwood does not disclose interactively designating a motif extraction range (page 4 of the Office Action). Regarding Kawashini, the Examiner asserts that in column 4, lines 4-35, Kawanishi, discloses the motif extracting means for extracting a motif based on the designated extraction range. However, referring to the portion pointed out by the Examiner, although Kawanishi discloses a technique to extract, as a motif, a part having a regularity characteristic in the gene arrangements based on a calculated score, in Kawanishi,

the motif extraction range is merely designated (set) automatically (column 4, lines 21-24). The Examiner also asserts that in column 11, lines 31-40, Marr discloses the concept of interactively entering commands for comparison among gene arrangements on a computer. However, Marr does not disclose or suggest interactively designating a motif extraction range. In other words, Marr merely discloses the concept of interactive command input. Therefore, the Applicants assert that no matter how a person skilled in the art had referred to the relied upon references or their combination, the present invention's patentably distinguishing feature, in which it is possible to interactively designate the motif extracting range from the gene arrangement information input as an object to be clarified, could not have easily been accomplished (i.e., the relied upon references do not render obvious the recitation, "operator interactively designating ... a motif extraction range in the input gene arrangement information").

Second, regarding the recitation, "adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information," the Examiner relies on Attwood, because Kawanishi and Marr do not disclose or suggest the recitations, "adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information." In contrast to Attwood, the idea of the present invention is the configuration of interactive motif extraction on an input gene arrangement, as the input gene arrangement is added to, based upon the interactive motif extraction. Attwood does not disclose or suggest adding to an input gene sequence a gene sequence retrieved from existing gene sequences that includes an interactively extracted motif of the input gene sequence. Such adding to the input gene sequence based upon the interactive motif extraction has a benefit of reutilizing an interactively designated motif extracted from the input gene information to be sequenced and improving a motif extracting efficiency for determining functions and structures of genes.

The Examiner appears to assert that the claims recite retrieving from a gene arrangement information database, which is not limited to be the same as the input gene information arrangement (page 4, third paragraph, of the Office Action). Further, the Examiner asserts that Attwood discloses using a motif database (input gene information arrangement) to retrieve sequences from a larger database, then adds the retrieved information to the motif database. The Examiner appears to rely on Attwood, page 417, column 2, 3rd paragraph, which discloses use of motif databases derived from a larger primary database, and asserts that a motif database is similar to the present invention's recitation, "input gene arrangement information." Further, Attwood, page 418, column 1, 2nd paragraph, discloses adding information from the new sequences to the initial motifs, which the Examiner asserts as similar to the

recitation, "adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information."

However, if one assumes that Attwood's sequence alignments is similar to the claimed "input gene arrangement information" and the conserved motifs excised therefrom are similar to the claimed "motif extracted from the input gene arrangement information," Attwood does not add the new sequence information to the sequence alignments as the input gene arrangement information. In contrast to the claimed present invention, Attwood adds the new sequence information to the extracted motifs (Attwood, page 418, column 1, 2nd paragraph).

Further, the claims clearly recite, "inputting at least one piece of gene arrangement information" from which a motif is interactively extracted, which differs from extracting a motif from a genetic database as the Examiner appears to be suggesting on page 4, 3rd paragraph, of the Action. Attwood, page 417, column 2, 3rd and 4th paragraphs, only disclose available motif databases and reduction of conserved motifs within alignments into single consensus expressions, which differs from the recitations, "interactively designating ... a motif extraction range in the input gene arrangement information" and "adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information." When performed iteratively, the claimed invention advantageously reutilizes an interactively designated motif extracted from the input gene information to be sequenced, which improves a motif extracting efficiency for determining functions and structures of genes.


The claimed combination of interactively designating a motif extraction and adding the retrieved extracted-motif-based gene arrangement information to the input gene arrangement information, is patentably distinguishing over the combination of Kwanishi, Attwood, and Marr. In view of the remarks and the claim amendments, withdrawal of the rejections of claims 2-9 and allowance of claim 2-9 is respectfully requested.

CONCLUSION

Finally, if there are any formal matters remaining after this response, the Examiner is requested to telephone the undersigned to attend to these matters.

Respectfully submitted,
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